

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hillman, Jennifer
Corley, Neil C.
Shah, Purvi
- (ii) TITLE OF THE INVENTION: NEW ANEXIN BINDING PROTEIN
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0354-2 DIV
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: PROSNON01
 - (B) CLONE: 2272281
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

PF-0354-2 DIV

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Met Lys Arg Asn Ser Pro Gln Lys Ile Lys Lys Arg Lys Asp Arg Arg
 1           5           10           15
Ala Lys Lys Gln Ser Phe Asp Asp Asn Asp Ser Glu Glu Leu Glu Asp
          20           25           30
Lys Asp Ser Lys Ser Lys Lys Thr Ala Lys Pro Lys Val Glu Met Tyr
          35           40           45
Ser Gly Ser Asp Asp Asp Asp Phe Asn Lys Leu Pro Lys Lys Ala
          50           55           60
Lys Gly Lys Ala Gln Lys Ser Asn Lys Lys Trp Asp Gly Ser Glu Glu
65           70           75           80
Asp Glu Asp Asn Ser Lys Lys Ile Lys Glu Arg Ser Arg Ile Asn Ser
          85           90           95
Ser Gly Glu Ser Gly Asp Glu Ser Asp Glu Phe Leu Gln Ser Arg Lys
          100          105          110
Gly Gln Lys Lys Asn Gln Lys Asn Lys Pro Gly Pro Asn Ile Glu Ser
          115          120          125
Gly Asn Glu Asp Asp Asp Ala Ser Phe Lys Ile Lys Thr Val Ala Gln
          130          135          140
Lys Lys Ala Glu Lys Lys Glu Arg Glu Arg Lys Lys Arg Asp Glu Glu
145          150          155          160
Lys Ala Lys Leu Arg Lys Leu Lys Glu Lys Glu Glu Leu Glu Thr Gly
          165          170          175
Lys Lys Asp Gln Ser Lys Gln Lys Glu Ser Gln Arg Lys Phe Glu Glu
          180          185          190
Glu Thr Val Lys Ser Lys Val Thr Val Asp Thr Gly Val Ile Pro Ala
          195          200          205
Ser Glu Glu Lys Ala Glu Thr Pro Thr Ala Ala Glu Asp Asp Asn Glu
          210          215          220
Gly Asp Lys Lys Lys Lys Asp Lys Lys Lys Lys Lys Gly Glu Lys Glu
225          230          235          240
Glu Lys Glu Lys Glu Lys Lys Lys Gly Pro Ser Lys Ala Thr Val Lys
          245          250          255
Ala Met Gln Glu Ala Leu Ala Lys Leu Lys Glu Glu Glu Glu Arg Gln
          260          265          270
Lys Arg Glu Glu Glu Glu Arg Ile Lys Arg Leu Glu Glu Leu Glu Ser
          275          280          285
Lys Pro
          290

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2272281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CTGTTCCAGT GCGCGGGTCT GTGGAGAGCC GGGTGCGAGC GGCGGCAGCA CGAGGGGAAA      60
AGAGCTGAGC GGAGACCAAA GTCAGCCGGG AGACAGTGGG TCTGTGAGAG ACCGAATAGA      120
GGGGCTGGGG CCACGAGCGC CATTGACAAG CAATGGGGAA GAAACAGAAA AACAAGAGCG      180
AAGACAGCAC CAAGGATGAC ATTGATCTTG ATGCCTTGGC TGCAGAAATA GAAGGAGCTG      240
GTGCTGCCAA AGAACAGGAG CCTCAAAAGT CAAAAGGGAA AAAGAAAAAA GAGAAAAAAA      300
AGCAGGACTT TGATGAAGAT GATATCCTGA AAGAACTGGA AGAATTGTCT TTGGAAGCTC      360
AAGGCATCAA AGCTGACAGA GAAACTGTTG CAGTGAAGCC AACAGAAAAC AATGAAGAGG      420
AATTCACCTC AAAAGATAAA AAAAAGAAAG GACAGAAGGG CAAAAAACA GAGTTTGTAT      480

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GATAATGATA GCGAAGAATT GGAAGATAAA GATTCAAAAT CAAAAAAGAC TGCAAAACCG 540
AAAGTGGAAA TGTACTCTGG GAGTGATGAT GATGATGATT TTAACAAACT TCCTAAAAAA 600
GCTAAAGGGA AAGCTCAAAA ATCAAATAAG AAGTGGGATG GGTCAGAGGA GGATGAGGAT 660
AACAGTAAAA AAATTAAAGA GCGTTCAAGA ATAAATTCTT CTGGTGAAAAG TGGTGATGAA 720
TCAGATGAAT TTTTGCAATC TAGAAAAGGA CAGAAAAAAA ATCAGAAAAA CAAGCCAGGT 780
CCTAACATAG AAAGTGGGAA TGAAGATGAT GACGCCTCCT TCAAAATTAA GACAGTGGCC 840
CAAAAGAAGG CAGAAAAGAA GGAGCGCGAG AGAAAAAAGC GAGATGAAGA AAAAGCGAAA 900
CTGCGGAAGC TGAAAGAAAA AGAAGAGTTA GAAACAGGTA AAAAGGATCA GAGTAAACAA 960
AAGGAATCTC AAAGGAAATT TGAAGAAGAA ACTGTAAAAT CCAAAGTGAC TGTTGATACT 1020
GGAGTAATTC CTGCCTCTGA AGAGAAAGCA GAGACTCCCA CAGCTGCAGA AGATGACAAT 1080
GAAGGAGACA AAAAGAAGAA AGATAAGAAG AAAAAGAAAG GAGAAAAGGA AGAAAAAGAG 1140
AAAGAGAAGA AAAAAGGACC TAGCAAAGCC ACTGTTAAAG CTATGCAAGA AGCTCTGGCT 1200
AAGCTTAAAG AGGAAGAAGA AAGACAGAAG AGAGAAGAGG AAGAACGTAT AAAACGCTT 1260
GAAGAATTAG AAAGCAAGCC GTAAGCACAA GGAACCGTTT GGAACCCAGA CAAAAGAGC 1320
AAGGGCACAG GCAAGACACC AAACCAAGGG GCGGCCCCCG AATTAATGTA CCTCTTCGCA 1380
CCGGGACTTC CTTTCGGGGC CGTTCCTGCA AGCGGAACCA ATTTTCCTTA AAGG 1434

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1514949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Gly Gln Lys Gly Lys Lys Thr Ser Phe Asp Glu Asn Asp Ser Glu Glu
 1          5          10          15
Leu Glu Asp Lys Asp Ser Lys Ser Lys Lys Pro Ala Arg Pro Asn Ser
 20          25          30
Glu Val Leu Leu Ser Gly Ser Glu Asp Ala Asp Asp Pro Asn Lys Leu
 35          40          45
Ser Lys Lys Gly Lys Lys Ala Gln Lys Ser Thr Lys Lys Arg Asp Gly
 50          55          60
Ser Glu Glu Asp Glu Asp Asn Ser Lys Arg Ser Lys Glu Arg Ser Arg
 65          70          75          80
Val Asn Ser Ser Gly Glu Ser Gly Gly Glu Ser Asp Glu Phe Leu Gln
 85          90          95
Ser Arg Lys Gly Gln Lys Lys Asn Gln Lys Asn Lys Ser Val Pro Thr
100          105          110
Ile Asp Ser Gly Asn Glu Asp Asp Asp Ser Ser Phe Lys Ile Lys Thr
115          120          125
Val Ala Gln Lys Lys Ala Glu Lys Lys Glu Arg Glu Arg Lys Lys Arg
130          135          140
Glu Glu Glu Lys Ala Lys Leu Arg Lys Val Lys Glu Lys Glu Glu Leu
145          150          155          160
Glu Lys Gly Arg Lys Glu Gln Ser Lys Gln Arg Glu Pro Gln Lys Arg
165          170          175
Pro Asp Glu Glu Val Leu Val Leu Arg Gly Thr Pro Asp Ala Gly Ala
180          185          190
Ala Ser Glu Glu Lys Gly Asp Ile Ala Ala Thr Leu Glu Asp Asp Asn
195          200          205
Glu Gly Asp Lys Lys Lys Lys Asp Lys Lys Lys Lys Lys Thr Glu Lys
210          215          220
Asp Asp Lys Glu Lys Glu Lys Lys Lys Gly
225          230

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